## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/541.598	
Source:	IFWP	
Date Processed by STIC:	8/10/06	
· ·	7.7	

## ENTERED



**IFWP** 

RAW SEQUENCE LISTING DATE: 08/10/2006
PATENT APPLICATION: US/10/541,598 TIME: 09:54:22

```
3 <110> APPLICANT: Moses, Ashlee
             Frueh, Klaus
      5
             King, Jeffrey S.
             Hicks, James B.
             Raggo, Camilo
             Nelson, Jay
     10 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS OF KAPOSI'S SARCOMA (KS)
AND
             KS RELATED DISEASES
     11
    13 <130> FILE REFERENCE: 49321-142
     15 <140> CURRENT APPLICATION NUMBER: US 10/541,598
     16 <141> CURRENT FILING DATE: 2005-07-05
     18 <150> PRIOR APPLICATION NUMBER: US 60/438,343
     19 <151> PRIOR FILING DATE: 2003-01-06
    21 <150> PRIOR APPLICATION NUMBER: US 60/473,246
    22 <151> PRIOR FILING DATE: 2003-05-22
    24 <150> PRIOR APPLICATION NUMBER: PCT US04/00320
    25 <151> PRIOR FILING DATE: 2004-01-06
    27 <160> NUMBER OF SEQ ID NOS: 33
    29 <170> SOFTWARE: PatentIn version 3.3
    31 <210> SEQ ID NO: 1
    32 <211> LENGTH: 2035
    33 <212> TYPE: DNA
    34 <213> ORGANISM: homo sapiens
    37 <220> FEATURE:
    38 <221> NAME/KEY: CDS
    39 <222> LOCATION: (152)..(1240)
    41 <400> SEQUENCE: 1
    42 tgcaagtctg cagccagcag agctcacagt tgttgcaaag tgctcagcac taagggagcc
                                                                            60
    120
    46 cggaggtcat ttgattgccc gcctcagaac g atg gat ctg cat ctc ttc gac
                                                                           172
    47
                                          Met Asp Leu His Leu Phe Asp
    48
    50 tac tea gag eca ggg aac tte teg gae ate age tgg eca tge aac age
                                                                           220
    51 Tyr Ser Glu Pro Gly Asn Phe Ser Asp Ile Ser Trp Pro Cys Asn Ser
    54 age gae tge ate gtg gtg gae aeg gtg atg tgt eec aac atg eec aac
                                                                           268
    55 Ser Asp Cys Ile Val Val Asp Thr Val Met Cys Pro Asn Met Pro Asn
    56
    58 aaa agc gtc ctg ctc tac acg ctc tcc ttc att tac att ttc atc ttc
                                                                           316
    59 Lys Ser Val Leu Leu Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe
                           45
    62 gtc atc ggc atg att gcc aac tcc gtg gtg gtc tgg gtg aat atc cag
                                                                           364
    63 Val Ile Gly Met Ile Ala Asn Ser Val Val Val Trp Val Asn Ile Gln
```

64					60					65					70		
66	gcc	aag	acc	aca	ggc	tat	gac	acg	cac	tgc	tac	atc	ttg	aac	ctg	gcc	412
67	Ala	Lys	Thr	Thr	Gly	Tyr	Asp	Thr	His	Cys	Tyr	Ile	Leu	Asn	Leu	Ala	
68				75					80					85			
		_	_	ctg		_	_					_			_	_	460
	Ile	Ala	_	Leu	Trp	Val	Val		Thr	Ile	Pro	Val	-	Val	Val	Ser	
72			90					95					100				
		-	_	cac		_			_				_	_		_	508
	Leu		Gln	His	Asn	Gln	_	Pro	Met	Gly	Glu		Thr	Cys	Lys	Val	
76		105					110					115					
				atc													556
		His	Leu	Ile	Phe		He	Asn	Leu	Phe		Ser	Ile	Phe	Phe		
	120					125					130					135	
	_	-	_	agc		_	_										604
	Tnr	Cys	мет	Ser		Asp	Arg	Tyr	ьeu		тте	Tnr	Tyr	Pne		Asn	
84	200	~~~	200	200	140		222	- <del></del>	~+ ·	145		~+~	~+~	<b>+~</b> a	150	~+~	650
				agc			_	_	_	_	_	_	_	_		_	652
88	TILL	PIO	Ser	Ser 155	Arg	пуs	пуъ	Mec	160	Arg	Arg	vai	vai	165	TIE	ьеи	
	ata	taa	cta	ctg	acc	ttc	tac	ata		ata	cat	~ ~ ~	200		tac	cta	700
				Leu													700
92	• • • •		170	200	u	1110	CyD	175	DCI	<b></b> cu	110	1101	180		- 1 -	<b>D</b> Cu	
	aaσ	acc		acg	tct	aca	t.cc		aat	gag	acc	tac		caa	t.cc	ttc	748
	_		-	Thr									_				•
96	•	185					190					195	- 2				
98	tac	ccc	gag	cac	agc	atc	aaq	gag	tqq	ctq	atc	qqc	atq	qaq	ctq	qtc	796
									Trp								
			GIU				LL y S						1100	O I U	neu	vaı	
100	200		GIU		Jer	205	_	014			210	_	Mee	Olu	пец	215	
102	tcc	) : gtt	gto	: ttg	ggc	205 ttt	geo	gtt			210 tcc	att	ato	gct	gto	215 ttc	844
102	tcc	) : gtt	gto	: ttg	ggc	205 ttt	geo	gtt			210 tcc	att	ato	gct	gto	215	844
102	tco Ser	) : gtt	gto	: ttg	ggc	205 ttt Phe	geo	gtt			210 tcc Ser	att	ato	gct	gto	215 ttc Phe	844
102 103 104 106	tco Ser L tao	ogtt Val	gto Val	ttg Leu	ggc Gly 220	205 ttt Phe	gcc Ala	gtt Val	Pro	Phe 225 gcg	210 tcc Ser	att Ile	ato Ile	gct Ala	gto Val 230	215 ttc Phe	844 892
102 103 104 106	tco Ser Ser tao Tyr	ogtt Val	gto Val	ttg Leu ctg	ggo Gly 220 gcc Ala	205 ttt Phe	gcc Ala	gtt Val	tcg Ser	Phe 225 gcg Ala	210 tcc Ser	att Ile	ato Ile	gct Ala	gto Val 230	215 ttc Phe	
102 103 104 106 103	tco Ser Ser tao Tyr	gtt gtt Val	gto Val c cto	ttg Leu ctg Leu 235	ggc Gly 220 gcc Ala	205 ttt Phe aga Arg	gco Ala gco Ala	gtt Val ato	tcg Ser 240	Phe 225 gcg Ala	210 tcc Ser tcc Ser	att att Ile agt	ato E Ile : gao	get Ala c cag c Glr 245	gto Val 230 ggag Glu	215 ttc Phe aag Lys	892
102 103 104 106 107	tco Ser tac Tyr Cac	gtt gtt Val tto Phe	gto Val c cto e Leu	ttg Leu g ctg Leu 235 c cgg	ggc Gly 220 gcc Ala	205 ttt Phe aga Arg	gcc Ala gcc Ala Ala	gtt Val ato	tcg Ser 240	Phe 225 gcg Ala	210 tcc Ser tcc Ser ser	att att Ile agt Ser	ato E Ile Gac Asp	gct Ala c cag Glr 245	gto Val 230 gag Glu	215 ttc Phe a aag Lys	
102 103 104 106 103 110	tco Ser tac Tyr Cac His	gtt gtt Val tto Phe	t gto l Val c cto e Leu c ago	ttg Leu g ctg Leu 235 c cgg	ggc Gly 220 gcc Ala	205 ttt Phe aga Arg	gcc Ala gcc Ala Ala	gtt Val atc Ile	tcg Ser 240 tcc	Phe 225 gcg Ala	210 tcc Ser tcc Ser ser	att att Ile agt Ser	ato e Ile gao Asp gto	get Alace cago Glr. 245	gto Val 230 gag Glu	215 ttc Phe aag Lys	892
102 103 104 106 107 108 110	2 tcc 3 Ser 4 Tyr 3 Cac 1 His	o gtt c gtt c tto c tto c Phe c ago	gtc Val c ctg Lev c ago Ser 250	c ttg Leu g ctg Leu 235 c cgg	ggc Gly 220 Ggc Ala Ala Lys	205 ttt Phe aga Arg	gcc Ala gcc Ala Ala atc	gtt Val atc atc ttc Phe 255	tcg Ser 240 tcc Ser	Phe 225 gcg Ala tac	210 tcc Ser tcc Ser ytcc Ser ytcc	att att Ile agt Ser Ser y gto	gac Asp Val	c gct e Ala c cag o Glr 245 c tto	gto Val 230 g gag n Glu ctt	215 ttc Phe aag Lys gtc	892 940
102 103 104 106 107 116 117 112	2 tcc 3 Ser 5 tac 7 Tyr 3 cac 1 His	y gtt Val C tto Phe ago Ser	gtc Val c ctg c ago c Ser 250 g ctg	c ttg ctg ctg Leu 235 ccgg Arg	ggc Gly 220 gcc Ala Lys	205 ttt Phe aga Arg atc Ile	gcc Ala gcc Ala atc	gtt Val atc Ile ttc 255	tcg Ser 240 tcc Ser ser gtg	Phe 225 gcg Ala tac Tyr ctg	210 tcc Ser tcc Ser val	atter Ile agter Ser y gto	gac Asr Val	c gct e Ala c cag c Glr 245 c ttc Phe	gtc Val 230 gag Glu ctt	215 ttc Phe aag Lys gtc Val	892
102 103 104 106 103 116 113 114 115	2 tcc 3 Ser 5 tac 7 Tyr 3 cac 1 His 2 tgc 5 Cys	gtt gtt Val c ttc Phe ago Ser tgg	gto Val c ctg E Leu c ago Ser 250 ctg	c ttg ctg ctg Leu 235 ccgg Arg	ggc Gly 220 gcc Ala Lys	205 ttt Phe aga Arg atc Ile	gcc Ala gcc Ala atc atc Ile	gtt Val a Ile tto Phe 255 gcg	tcg Ser 240 tcc Ser ser gtg	Phe 225 gcg Ala tac Tyr ctg	210 tcc Ser tcc Ser val	att att agt Ser y gto Val	g gto Val	c gct e Ala c cag c Glr 245 c ttc Phe	gtc Val 230 gag Glu ctt	215 ttc Phe aag Lys gtc	892 940
102 103 104 106 108 110 112 114 115	2 tcc 3 Ser 4 tac 7 Tyr 3 cac 1 His 2 tgc 5 Cys	gtt gtt Val ttc Phe ago Ser tgg	gto Val c cto e Leu c ago c Ser 250 cto o Leu	ttg Leu g ctg Leu 235 c cgg Arg	ggc Gly 220 Ala Ala Lys	205 c ttt Phe c aga Arg atc s Ile c cac	gcc Ala gcc Al	gtt Val ato Ile tto Phe 255 gcg	tcg Ser 240 tcc Ser gtg	Phe 225 gcg Ala tac Tyr ctg	210 tcc Ser tcc Ser Val	atter Ile agter Ser Ser Val	g gto Val 260 at co 116	get Alac cago Glr 245 tto Phe	gtc Val 230 g gag i Glu c ctt Leu tcc	215 ttc Phe y aag Lys gtc Val	892 940 988
102 103 104 106 108 110 112 114 115 116	E too Ser too Tyr Control  His Cys Cys Cys	gtt Val tto Phe cago Ser tgg Trp 265	c gtc L Val c ctc c ago c Ser 250 ctc c Leu	c ttg Leu g ctg Leu 235 c cgg Arg c Arg	ggc Gly 220 Ala Ala Lys tac Tyr	205 tttt Phe aga Arg Arg Atc His	gcc Ala gcc Al	gtt Val atc Ile ttc Phe 255 gcg Ala	tcg Ser 240 tcc Ser ggg Val	Phe 225 gcg Ala tac Tyr ctg Leu	210 E tcc Ser Ser Val	atter Ile agter Ser Ser Val	g gto Val 260 ato 116	get Alac cago Glr. 245 ttc. Phe	gtc Val 230 g gag i Glu c ctt E Leu tcc	215 ttc Phe aag Lys Val	892 940
102 103 104 106 107 112 114 115 116 118	2 tcc 3 Ser 4 5 tac 7 Tyr 3 cac 4 tgc 5 Cys 5 Cys 6 tcc 9 Leu	gtt gtt Val c tto phe c ago s Ser c tgg 265 g cao	c gtc L Val c ctc c ago c Ser 250 ctc c Leu	c ttg Leu g ctg Leu 235 c cgg Arg c Arg	ggc Gly 220 Ala Ala Lys tac Tyr	205 tttt Phe aga Arg atc Ile cac His	gcc Ala gcc Ala gcc Ala gcc Ala gcc Ile gtg Yal 270 acc Thr	gtt Val atc Ile ttc Phe 255 gcg Ala	tcg Ser 240 tcc Ser ggg Val	Phe 225 gcg Ala tac Tyr ctg Leu	210 tcc Ser Ser Val	atter Ile agter Ser Ser Val Val 275 cach His	g gto Val 260 ato 116	get Alac cago Glr. 245 ttc. Phe	gtc Val 230 g gag i Glu c ctt E Leu tcc	215 ttc Phe gaag Lys yal yal ttc The acg	892 940 988
102 103 104 106 103 114 112 114 118 118	2 tcc 3 Ser 4 5 tac 7 Tyr 3 cac His Cys 6 Cys 6 Cys 7 Cys 7 Cys 7 Cys 7 Cys 8 C	gtt Val C ttc Phe C ago S Ser C tgg C tgg C tgg His	c gtcl l Val c ctcl c ago c Ser 250 g ctcl c tao	c ttg ctg ctg Leu 235 cgg Arg ccc pro	ggc Gly 220 Ala Lys tac Tyr	205 tttt Phe aga Arg atc Ile cac His	gcc Ala gcc Ala gcc Ala gcc Ile gtg Val 270 acc Thr	gtt Val ato tto Phe 255 gcg Ala	tcg Ser 240 tcc Ser y gtg Val	Phe 225 gcg Ala tac Tyr ctg Leu	210 tcc Ser Ser Val	atter Ile agter Ser Ser Val Val 275 gac cach His	gac Asp Val 260 ato Ile S Ala	get Alac cago Glr 245 tto Phe tto Cto Leu	gtc Val 230 g gag Glu ctt Leu tcc Ser	215 ttc Phe gaag Lys gtc Val atc Ile acg Thr 295	940 988 1036
102 103 104 106 107 112 114 115 116 118 120 122	2 tcc 3 Ser 4 5 tac 7 Tyr 3 cac His Cys 6 Cys 6 Cys 7 Leu 9 280 2 gcc	tto Phe ago Ser tgg Caco His	c gtcl l Val c ctc e Leu c ago c Ser 250 c tcc c tao	c ttg ctg ctg Leu 235 ccgg Arg ccc pro	ggc Gly 220 Gly Gc Ala Lys Lys Tyr	205 tttt Phe aga Arg at Arg Ile cac His ttc Phe 285 cag	gcc Ala gcc Al	gtt Val atc ttc Phe 255 gcg Ala	tcg Ser 240 tcc Ser tcc Ser y gtg Val	Phe 225 Ala tac Tyr ctg Leu ctg	210 tcc Ser Ser Val Ctg Gag Glu 290 gtg	atter Ile agter Ser Ser Val Val Asp cace His	gac gac Asp yal 260 ato o Ile	c gct e Ala c cag c Glr 245 c ttc Phe c ttc c Leu c tgc	gtc Val 230 g gag Glu ctt Leu tcc Ser ttc	215 ttc Phe aag Lys yal val atc leacg Thr 295 aac	892 940 988
102 103 104 106 107 108 112 114 115 116 118 120 122 123	2 tcc 3 Ser 4 tac 7 Tyr 3 cac 4 tgc 5 Cys 6 Cys 6 Cys 6 Cys 7 Leu 9 Leu 9 Leu 9 Ser 9 Leu 9 Ser 9 Ser 1 tac 1 tac 1 tac 1 tac 1 tac 1 tac 1 tac 2 tac 2 tac 2 tac 3 tac 4 tac 6 tac 6 tac 6 tac 7 tyr 8 tac 8	tto Phe ago Ser tgg Caco His	c gtcl l Val c ctc e Leu c ago c Ser 250 c tcc c tao	c ttg ctg ctg Leu 235 ccgg Arg ccc pro	ggc Gly 220 Ala Lys tac Tyr	205 tttt Phe aga Arg atc s Ile cac His ttc Phe 285 a cag	gcc Ala gcc Al	gtt Val atc ttc Phe 255 gcg Ala	tcg Ser 240 tcc Ser tcc Ser y gtg Val	Phe 225 gcg Ala tac Tyr ctg Leu ctg Leu Leu Leu Leu	210 tcc Ser tcc Ser Val Ctg	atter Ile agter Ser Ser Val Val Asp cace His	gac gac Asp yal 260 ato o Ile	c gct e Ala c cag c Glr 245 c ttc Phe c ttc c Leu c tgc	gtc Val 230 gag Glu ctt Leu tcc Ser ttc Phe	215 ttc Phe aag Lys yal atc Ile acg Thr 295 aac Asn	940 988 1036
102 103 104 106 107 108 112 114 115 116 122 123 124	2 tcc 3 Ser 4 tac 7 Tyr 3 cac 4 tgc 5 Cys 5 Cys 6 Cys 6 Cys 6 Cys 7 Leu 9 Leu 9 Leu 9 Leu 9 Ser 9 Leu 9 Ser 9 Ser 1 tac 1 tac 9 Cys 1 tac 1	tto tto Phe ago Ser Try cao His	c gtcl c ctcl c ago c Ser 250 ctcl c tao c tao c tao f cat i His	c ttg ctg ctg Leu 235 ccgg Arg ccc pro	ggc Gly 220 Ala Ala Lys tac Tyr	205 tttt Phe aga Arg atc s Ile cac His ttc Phe 285 cag	gcc Ala gcc Al	gtt Val atc atc ttc Phe 255 gcc Ala tgc Cys	tcg Ser 240 tcc Ser y gtg Val cgg Arg	Phe 225 gcg Ala tac Tyr ctg Leu ctg Leu 305	210 tcc Ser tcc Ser Val ctc Gag Gag Gag Val	atter Ile agter Ser grand Aspendent	gac gac Asp yal 260 ato o Ile o gco s Ala	get Alac cago Glr 245c tto Phe Phe cto Leu tgo Cys	gto Val 230 gag Glu ctt Leu tcc Ser ttc Val 310	215 ttc Phe aag Lys yal atc Ile acg Thr 295 aac Asn	940 988 1036
102 103 104 106 107 108 112 114 115 116 122 123 124 126	2 tcc 3 Ser 4 tac 7 Tyr 3 cac 1 tgc 6 Cys 6 Cys 6 Cys 6 Cys 7 Tyr 8 tgc 8 ctc 8 ctc 9 Leu 9 Leu 9 Leu 9 Ccc 8 Ala	tto tto Phe ago Ser Try 269 Cao His Cao Let	c gtcl l Val c ctc c ago c Ser 250 ctc c tao c tao c tao c tao c tao c tao	c ttg ctg ctg Leu 235 ccgg Arg cca pro ctg ttg ttg ttg ttg ttg ttg ttg ttg ttg	ggc Gly 220 Ala Ala Lys tac Tyr cct Pro	205 tttt Phe aga Arg atc s Ile cac His ttc Phe 285 cag cag cac ttc	gcc Ala gcc Al	gtt Val atc atc ttc 255 gcc Ala Cys ctc atc	tcg Ser 240 tcc Ser y tcg Val cgg Arg	Phe 225 gcg Ala tac Tyr ctg Leu ctg Leu 305 aac	210 tcc Ser tcc Ser Val Ctc Glu 290 gtc Val Val tac	atter Ile agter Ser grand Asprand Aspr	gac gac Asp yal 260 atc o 11e gcc s Ala	get Alac cago Glr 245 ctto Phe Ctc tto Ctc tgc Cys	gto Val 230 gag Glu ctt Leu tcc Ser ttc Ser ttc Ser ttc Ser ttc Ser ttc Ser ttc Ser ttc Ser ttc Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	215 ttc Phe aag Lys Val atc Ile acg Thr 295 aac Asn	940 988 1036
102 103 104 106 107 108 112 114 115 116 122 123 124 126	2 tcc 3 Ser 4 tac 7 Tyr 3 cac 4 tgc 5 Cys 6 Cys 6 Cys 6 Cys 8 Ala	tto tto Phe ago Ser Try 269 Cao His Cao Let	c gtcl l Val c ctc c ago c Ser 250 ctc c tao c tao c tao c tao c tao c tao	c ttg ctg ctg Leu 235 ccgg Arg cca pro ctg ttg ttg ttg ttg ttg ttg ttg ttg ttg	ggc Gly 220 Ala Ala Lys tac Tyr cct Pro	205 tttt Phe aga Arg atc s Ile cac His ttc Phe 285 cag cag cac ttc	gcc Ala gcc Al	gtt Val atc atc ttc 255 gcc Ala Cys ctc atc	tcg Ser 240 tcc Ser y tcg Val cgg Arg	tac Tyr ctg Leu 305 aac Asn	210 tcc Ser tcc Ser Val Ctc Glu 290 gtc Val Val tac	atter Ile agter Ser grand Asprand Aspr	gac gac Asp yal 260 atc o 11e gcc s Ala	get Alac cago Glr 245 ctto Phe Ctc tto Ctc tgc Cys	gto Val 230 gag Glu ctt Leu tcc Ser tto Phe Val 310 g ctg	215 ttc Phe aag Lys yal atc Ile acg Thr 295 aac Asn	940 988 1036

131 Lys Ala Phe Ile Phe Lys Tyr Ser Ala Lys Thr Gly Leu Thr Lys Leu   330   340   340   335   340   341   345   345   345   355   355   346   345   355   355   348   382   acc aaa tga tctgcctgg agaggctctg ggacgggttt acttgtttt   1280   138   agc acc aaa tga tctgccctgg agaggctctg ggacgggttt acttgtttt   1280   139 Ser Thr Lys   140 360   142 gaacaggtg atgggcccta tggtttcta gagcaaagca   aagtagcttc gggtcttgat   1340   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   146   14
134 acc gat gcc tcc aga gtc tca gag acg gag tac tct gcc ttg gag cag 135 Tle Asp Ala Ser Ary Val Ser Glu Thr Glu Tyr Ser Ala Leu Glu Gln 136
135 1le Asp Ala Ser Arg Val Ser Glu Thr Glu Tyr Ser Ala Leu Glu Gln 315 350 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 355 350 350
136
139 Ser Thr Lys 140 360 142 gaacagggtg atgggcccta tggttttcta gagcaaagca aagtagcttc gggtcttgat 1340 144 gcttgagtag agtgaagagg ggagcacgtg cccctgcat ccattctct tttctcttga 1400 146 tgacgcagct gtcatttgct tgtgcgtgct gacagttttg caacaggcag agctgtgtcg 1460 148 cacagcagtg ctgtgcgtca gagccagctg aggacaggct tcctgtaagat 1520 150 aggatttct gtgtttcctg aatttttat atggtgattt gtatttaaat tttaagactt 1580 152 tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat attttaaata 1640 154 ttgtttggga ggcatagtgc tgacatatat tcagagtgt ttggatttaa ggttagcgtg 1700 156 acttcagttt tgactaagga tgacactaat tgtagttgt tttgaaatat atattaatat 1760 158 aatatatata aatataaaa tatatgccag tcttggctga aatgttttat ttaccatagt 1820 160 tttatatctg tgtggtgttt tgtaccggca cgggatatgg aacgaaaact gctttgaat 1880 162 gcagtttgtg acattaatag tattgtaaag ttacttta aaataaacaa aaaactgtc 1940 164 tggactgcaa atctgcacac acaacgaaca gttgcattc agagagttct ctcaatttg 2000 166 aagttattt tttttaataa agatttttg ttcct 2002 167 <211> LENGTH: 362 171 <212> TYPE: PRT 172 <213> ORGANISM: homo sapiens 174 <400> SEQUENCE: 2 176 Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 177 17 1 5 10 15 180 Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val 181 20 25 30 184 Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Tyr Thr Leu Ser 185 35 40 45 188 Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val 189 50 60 190 Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His 193 65 70 75 80 194 Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr 197 85 90 200 Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met 201 100 105 110 204 Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu 205 115
139   Ser Thr Lys   140   360   360   142   360   360   142   360   360   142   360   360   142   360   360   144   gettgagtag agtgaagagg gagcacgtg cccctgcat   ccattetete   tttetettga   1400   146   tgacgcaget gteatttge   tgtgegtget   gacagtttg   ccaccaggcag agctgtgteg   1460   148   cacagcagget gttgttetete   gagcagetg   gacaggettge   1460   148   cacagcagtg   ctgtgegtca   gagcacgtg   gacaggettgecgaet   tettgtaagat   1520   150   aggatttete   tgtgttteetg   aattittat   atggtgattg   tgtatttaaat   tttaagagett   1580   152   tatttteetca   ctattggtgt   accttataaat   tgtatttgaa   agttaaatat   attitaaata   1640   154   ttgtttggga   ggcatagtge   tgacatatat   teagaggtgt   tttgaaatat   attitaaata   1760   156   acttcagttt   tgacataaga   tgacatatat   teagaggtgt   tttgaaatat   tatataatata   1760   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170   170
142       gaacagggtg atgggcccta tggttttcta gagcaaagca aagtagcttc gggtcttgat       1340         144       gcttgagtag agtgaagagg gagcacgtg cccctcgat ccattctct tttctcttga       1460         146       tgacgcagct gtcatttggc tgtgctggct gacagttttg caacaggcag agctgtgtcg       1460         148       cacagcagtg gtcatttggc tgtgctggact gacagttttg caacaggcag agctgtgtcg       1460         148       cacagcagtg ctgtgctga gagccagctg aggacaggct tgcctggact tctgtaagat       1520         150       aaggattttct gtgtttcctg aatttttata taggtgattt gtatttaaat tttaagatt       1580         152       tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat tttaagtgtg       1700         156       atttttctca ctattggtgt ctgacataat tcaaggtgtt gtagttttaa ggttagcgtg       1700         156       acttcagttt tgactaagg tgacactaat tgttagctgt tttgaaatta ttatatata       1760         158       aatatataa aatatataaa atatagccag tcttggctga aatgtttat ttaccatagt       1820         160       tttatatctg tgtggtgttt tgtaccggac cgggatatgg aacgaaaca gcttgtatt       1880         162       gcagtttgtg acattaataa tattgtaaag ttacattta aaataaacaa aaaactgtc       1940         164       ttgaccgcaa atctgacac acaacgaaca gttgcattc       aggaggtct ctcaatttg         164       ttgactgtas       1820         162       210 NO: 2       2         17       21 No
144 gcttgagtag agtgaagagg ggagcacgtg cccctgcat       cccttgctc tttctct tttctcttga       1400         146 tgacgcagct gtcatttggc tgtgcgtgct gacagttttg       caacagcaga agctgtgtg       1460         148 cacagcagtg ctgtgcgtca gagcagctg gagcaggct tgcctggact tctgtaagat       1520         150 aggattttct gtgtttcctg aatttttat attgtgtattt       tgcctggact tcttgtaagat       1520         152 tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat       attttaaat       1640         154 ttgtttgggg ggcatagtgc tgacatatat       tcagagtgtt gtagttttaa ggttagcgtg       1700         156 acttcagttt tgactaagga tgacaccatat tgttagctgt       tttgagttttat tatatatata       1760         158 aatatataa aatatataaa tatatgcag tcttggctga       aatgttttat ttaccatagt       1820         160 tttatatctg tgtggtgttt tgtaccggca cgggatatg       aacgaaaact gctttgtaat       1880         162 gcagtttgtg acattaatag tattgtaaag ttacattta       aaataaacaa aaaactgtc       1940         164 tggactgcaa atctgcacac acaacgacaa gttgcattc       agagagtct ctcaatttg       2000         164 tggactgcaa atctgcacac acaacgacaa gttgtcattc       agagagtct ctcaatttg       2000         165 aggattgtgg acattaatag tattgtaaag ttacattta       aaataaacaa aaaactgtc       1940         164 tggactgcag gacattagtge       tgtgcattc       aagaggtct       ctcaatttg         160 tttaatctgtgt       tgtgctgtatt       tgctgtattc       tccaattg
146       tgaagcagct gtcatttgge tgtgcgtget gacagttttg       caacaggcag agctgtgcg       1460         148       cacagcagtg ctgtgcgtca gagccagctg aggacaggct       tgcctggact tctgtaagat       1520         150       aggattttct gtgtttcctg aatttttat atggtgatt       gtatttaaat tttaagactt       1580         152       tattttctca ctattggtgt accttataaa tgtatttgaa       agttaaatat       1580         152       tattttctca ctattggtgt       tacttaaaa       1640         154       ttgtttgtggaggcatagtg       tgacataatat       1640         156       acttcagtt       tgacataatat       tctaagtgtgt       1700         158       aatatatata       aatattaaa       tatataccag       1820         160       tttatatctg tgtggtgtt       tgtaccggaa       cgggattgg       aacgaaaact       1820         160       tttatatctg tgtggtgtt       tgtaccggaa       cgggattgg       aacgaaaact       gttttgtaat       1880         162       gagtttgtg       acattaatag       tatttptaaag       ttacatttta       aaacgaaaact       gttttgtaat       1880         162       tggatttgtg       acattaatag       tatttpaaat       1820       1820       1820         164       tgagctgtat       tgtagtttaatat       tattattaaa       1820       1820       1
148       cacagcagtg       ctgtgcgtca       gagaccagctg       aggaccagctt       tgcctggact       tctgtaagat       1520         150       aggattttct       gtgtttcctg       aatttttat       atggtgattt       gtatttaaat       ttttaaat       1580         152       tattttctca       ctattggtg       aacttataaa       tgtatttaaa       agttaaata       ttttaaat       1640         154       ttgttttggg       ggcataatat       tcagagtgt       gtatttaa       atttaaata       1770         156       acttcagttt       tgacaactaat       ttgtagctg       tttgaaatta       ttaatataa       1760         158       aaataatata       aaataataaa       tatattgcaag       tcttggctg       aatgtttta       1760         160       ttatatctg       tgtggttt       tgtaactggaa       aaatgatttg       1820         160       ttatatataa       tatttgtaaag       ttacattta       aaatgattg       1820         161       ttatatatataa       tatttgtaaag       ttacattta       aagaggttt       ttacattta       1820         164       tgacgctgaa       acttgaataa       gatttgtatta       aagaagttt       2000       2035         164       tgacgtgts       acttgattaaag       ttacattta       aagagattta       tctaat
150 aggatttet gtgtttectg aatttttat atggtgattt gtattaaat tttaagactt 1580 152 tattttetea etattggtg accttataaa tgtatttga agttaaatat atttaaata 1640 154 ttgtttggga ggcatagtge tgacatatat teagagtgtt gtagttttaa ggttagegtg 1700 156 actteagttt tgactaagga tgacactaat tgttagetgt tttgaaatta tatatatat 1760 158 aatatata aatatataa tatatgecag tettggetga aatgttttat ttaecatagt 1820 160 tttatatetg tgtggtgttt tgtaceggea egggatatgg aacgaaacat getttgtaat 1880 162 geagtttgg acattaatag tattgtaaag ttaecattta aaataaacaa aacactgte 1940 164 tggactgeaa atctgecaca cacaacgaaca gttgeattte agaagagte eteaattgt 2000 166 aagttattt tttttaataa agattttgt tteet 2005 169 <210 > SEQ ID NO: 2 170 <211 > LENGTH: 362 171 <212 > TYPE: PRT 172 <213 > ORGANISM: homo sapiens 174 <400 > SEQUENCE: 2 176 Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 177 1
152 tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat attttaata
154 ttgtttggga ggcatagtgc tgacatatat tcagagtgtt gtagtttaa ggttagcgtg   1700   156 acttcagttt tgactaagga tgacactaat tgttagctgt   1700   158 actatatatatatatatatatatatatatatatatatat
156 acttcagttt tgactaagga tgacactaat tgttagetgt tttgaaatta tatatatata
158 aatatatata aatatataaa tatatgccag tettggctga aatgtttat ttaccatagt 1820 160 tttatatctg tgtggtgttt tgtaccggca cgggatatgg aacgaaaact gctttgtaat 1880 162 gcagtttgtg acattaatag tattgtaaag ttacatttta aaataaacaa aaaactgtc 1940 164 tggactgcaa atctgcacac acaacgaaca gttgcattc agagagtct ctcaatttgt 2000 166 aagttattt tttttaataa agattttgt ttcct 2010 169 <210 > SEQ ID NO: 2 170 <211 > LENGTH: 362 171 <212 > TYPE: PRT 172 <213 > ORGANISM: homo sapiens 174 <400 > SEQUENCE: 2 176 Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 17 1 5 10 15 180 Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val 21 25 184 Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser 35 40 45 188 Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val 189 50 55 60 192 Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His 193 65 70 75 80 196 Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr 95 95 200 Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met 100 105 110 204 Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu 205 115
160 tttatatctg tgtggtgttt tgtaccggca cgggatatgg aacgaaaact gctttgtaat 1880 162 gcagtttgtg acattaatag tattgtaaag ttacatttta aaataacaa aaaactgttc 1940 164 tggactgcaa atctgcacac acaacgaaca gttgcatttc agagagttct ctcaatttgt 2000 2035 166 aagttattt tttttaataa agattttgt ttcct 2005 2035 169 <210 > SEQ ID NO: 2 170 <211 > LENGTH: 362 171 <212 > TYPE: PRT 172 <213 > ORGANISM: homo sapiens 174 <400 > SEQUENCE: 2 176 Met Asp Leu iis Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 15 15 180 11e Ser Trp Pro Cys Asn Ser Ser Asp Cys Iie Val Val Asp Thr Val 181 20 25 30 30 184 Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser 185 35 40 45 11e Gly Met 11e Ala Asn Ser Val 189 50 55 60 60 192 Val Val Trp Val Asn Iie Gln Ala Lys Thr Thr Gly Tyr Asp Thr His 193 65 70 70 75 80 95 95 10 10 10 10 10 10 10 10 10 10 10 10 10
162 gcagtttgtg acattaatag tattgtaaag ttacatttta aaataaacaa aaaactgttc 1940 164 tggactgcaa atctgcacac acaacgaaca gttgcattc agagagttct ctcaatttgt 2000 166 aagttatttt ttttaataa agattttgt ttcct 2035 169 <210
164 tggactgcaa atctgcacac acaacgaaca gttgcattc agagagttct ctcaatttgt 2000 166 aagttatttt tttttaataa agatttttgt ttcct 2035 169 <210
166 aagttattt tttttaataa agatttttgt ttctt
169 <210 > SEQ ID NO: 2 170 <211 > LENGTH: 362 171 <212 > TYPE: PRT 172 <213 > ORGANISM: homo sapiens 174 <400 > SEQUENCE: 2 176 Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 15 177 1
170
171
172
174
176 Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp 177 1 180 Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val 181
177 1
180
181       January 1       20       181       25       30       30       30       30       30       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31       31
184       Met       Cys       Pro       Asn       Met       Pro       Asn       Lys       Ser       Val       Leu       Leu       Tyr       Thr       Leu       Ser         185
185       35       40       45         188 Phe
188       Phe       Ile       Tyr       Ile       Phe       Ile       Phe       Val       Ile       Gly       Met       Ile       Ala       Asn       Ser       Val         189       50       50       55       55       60       60       Tyr       Asp       Thr       His         192       Val       Val       Trp       Val       Asp       Ile       Ala       Lys       Thr       Gly       Tyr       Asp       Thr       His         193       65       65       70       70       70       75       75       70       80         196       Cys       Tyr       Ile       Leu       Asn       Leu       Ala       Ala       Asp       Leu       Trp       Val       Leu       Thr         197       7       110       100       100       105       105       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110       110 <td< td=""></td<>
189       50
192 Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His 193 65
193 65
196 Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr 197
197
200 Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met 201
201 100 105 110 204 Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu 205 115 120 125
204 Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu 205 115 120 125
205 115 120 125
· 2 /24 /14 /
209 130 135 140
212 Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
213 145 150 155 160
216 Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
217 165 170 175

220 Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn 221 180 185 190	
224 Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp 225 195 200 205	
228 Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro	
229 210 215 220	
232 Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser	
233 225 230 235 240	
236 Ala Ser Ser Asp Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser	
237 245 250 255 240 Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val	
240 Tyl Val Val Val File Bed Val Cys Tip Bed Flo Tyl His Val Ala Val 241 260 265 270	
244 Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg	
245 275 280 285	
248 Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser	
249 290 295 300	
252 Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg	
253 305 310 315 320	
256 Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala	
257 325 330 335	
260 Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr	
261 340 345 350	
264 Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys	
265 355 360 268 <210> SEQ ID NO: 3	
269 <211> LENGTH: 1421	
270 <212> TYPE: DNA	
271 <213> ORGANISM: homo sapiens	
274 <220> FEATURE:	
275 <221> NAME/KEY: CDS	
276 <222> LOCATION: (115)(1092)	
278 <400> SEQUENCE: 3	
279 ggcgagggag gaggaagaag cggaggaggc ggctcccgcg ctcgcagggc cgtgccacct	
2,) ggcgagggag gaggaagaag cgggagga ggcccccgcg cccgcagggc cgcgccaccc	60
281 gcccgccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg	60 117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg	
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282 Met 283 1 285 ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg	
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282  Met 283  1 285 ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg	117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	<ul><li>117</li><li>165</li><li>213</li></ul>
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	117
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282  283  285 ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg	<ul><li>117</li><li>165</li><li>213</li></ul>
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	<ul><li>117</li><li>165</li><li>213</li><li>261</li></ul>
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	<ul><li>117</li><li>165</li><li>213</li></ul>
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	<ul><li>117</li><li>165</li><li>213</li><li>261</li></ul>
281 gcccgcccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 282	<ul><li>117</li><li>165</li><li>213</li><li>261</li></ul>

302	Δla	Val	Δla	Glv	Glv	Δla	Ara	Met	Pro	Cvs	Δla	Glu	T.e.ii	Val	Ara	Glu	
303	1120	• • • • • • • • • • • • • • • • • • • •	1114	O. J	70	1124	9		110	75	mu	Olu	Dea	vul	80	Ozu	
305	ccg	ggc	tgc	ggc	tgc	tgc	tcg	gtg	tgc	gcc	cgg	ctg	gag	ggc	gag	gcg	405
306	Pro	Gly	Cys	Gly	Cys	Cys	Ser	Val	Cys	Ala	Arg	Leu	Glu	Gly	Glu	Ala	
307				85					90					95			
								tgc									453
	Cys	Gly		Tyr	Thr	Pro	Arg	Cys	Gly	Gln	Gly	Leu	_	Cys	Tyr	Pro	
311			100					105					110				501
		_				_		ctg	_		_	_	_				501
314	пір	115	GIY	ser	GIU	Leu	120	Leu	GIII	Ala	ьеи	125	Met	СТУ	GIU	GIY	
	act		gag	aag	cac	caa		gcc	aaa	tat	aac		age	cca	gag	cad	549
							_	Ala				-		-		-	313
	130	-1-		-2-	5	135				-1-	140					145	
321	gtt	gca	gac	aat	ggc	gat	gac	cac	tca	gaa	gga	ggc	ctg	gtg	gag	aac	597
								His									
323					150					155					160		
								atg									645
	His	Val	Asp		Thr	Met	Asn	Met		Gly	Gly	Gly	Gly	Ser	Ala	Gly	
327				165					170					175			
								atg									693
	Arg	гàг		Leu	ьys	ser	GLY	Met	ьys	GIU	Leu	Ala		Pne	Arg	GIU	
331	224	ata	180	asa	asa	a 2 a	000	185 cag	ata.	~~~	224	aat	190	224	ast	a2a	741
	_	_			_			Gln	_		_			_			741
335	шуо	195	****	0.14	01	1115	200	0111	1100	Ory	цу	205	OLY	цуз	1115	1115	
	ctt		ctq	qaq	qaq	ccc		aag	ctq	cqa	cca		cct	qcc	aqq	act	789
								Lys									
	210	_				215	_	_			220					225	
341	CCC	tgc	caa	cag	gaa	ctg	gac	cag	gtc	ctg	gag	cgg	atc	tcc	acc	atg	837
342	Pro	Cys	Gln	Gln	Glu	Leu	Asp	Gln	Val	Leu	Glu	Arg	Ile	Ser	Thr	Met	
343					230					235					240		
								cct	_						-		885
	Arg	ьeu	Pro		GIU	Arg	GIY	Pro		GIU	His	Leu	Tyr		Leu	HIS	
347	atc	000	220	245	a a c	224	cat	ggc	250 ct c	tac	220	ata	222	255	tac	224	933
				_	_	_		Gly	_					_	_	_	933
351			260	Cy D	p	_,,		265	Dea	- 7 -	11011	<b></b>	270	0111	Cyb	Д, О	
	atq	tct		aac	qqq	caq	cqt	ggg	qaq	tgc	taa	tat		aac	ccc	aac	981
								Gly									
355		275			_		280	_		-	-	285					
357	acc	ggg	aag	ctg	atc	cag	gga	gcc	ccc	acc	atc	cgg	ggg	gac	CCC	gag	1029
358	Thr	Gly	Lys	Leu	Ile	Gln	Gly	Ala	Pro	Thr	Ile	Arg	Gly	Asp	Pro	Glu	
	290					295					300					305	
								cag									1077
	Cys	His	Leu	Phe		Asn	Glu	Gln	Gln		Ala	Arg	Gly	Val		Thr	
363			_ 4		310					315					320		
					tag	acco	gcago	cca g	gccgg	gtgc	et go	gege	ccct	g cc	cccc	gccc	1132
366	GIU	arg	Met	GIN													

VERIFICATION SUMMARYDATE: 08/10/2006PATENT APPLICATION: US/10/541,598TIME: 09:54:23

Input Set : A:\49321-142 SEQ LIST.txt
Output Set: N:\CRF4\08102006\J541598.raw

٠, .